REMARKS

Pending Claims

Claims 3-7, 9, 11, 13, 15 and 28 are currently pending. Claims 12, 14, 18, 20, 21, 23-24 and 27 were canceled in the preliminary amendment. By this amendment, claims 1, 2, 8, 10, 16-17, 19, 22, and 25-26 have been canceled, and claims 3, 5, 9, and 11 have been amended herein. Claims 13, 15 and 28 have been withdrawn from consideration by the Examiner as being drawn to non-elected inventions. Claims 3-7, 9 and 11 are currently being examined on the merits.

Election/Restrictions

Applicants wish to reiterate their traversal of the election and restrictions imposed by the Examiner, for the reasons already made of record in their Response to the Restriction Requirement of June 24, 2002, which response was timely filed on August 26, 2002.

Rejoinder of Method Claims

Applicants submit that claims 13 and 15 (drawn to methods of detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide of claim 11) are methods of using the polynucleotides recited in claim 11, and that claim 28, drawn to a method of toxicity testing, is also a method of using the polynucleotides recited in claim 11. They remind the Examiner that these claims should be examined together with claims 3-7, 9 and 11, which are currently under consideration, per the Commissioner's Notice in the Official Gazette of March 26, 1996, entitled "Guidance on Treatment of Product and Process Claims in light of *In re Ochiai, In re Brouwer* and 35 U.S.C. § 103(b)" which sets forth the rules, upon allowance of product claims, for rejoinder of process claims covering the same scope of products

Claim Objections

Claims 3, 5, 9 and 11 have been amended to delete unelected subject matter, and Claims 3 and 9 have been amended to recite subject matter formerly recited in claim 3, from which claims 3 and 9 formerly depended. No new matter is added thereby.

Applicants therefore respectfully request that the Examiner withdraw the Objections in paragraph 11 of the Office Action currently under response.

Rejection of Claims 3, 6, 7 and 9 under 35 U.S.C. section 102(e) under Fearon *et al.* (U.S. Patent No. 5,981,481

Claim 3 as it is currently pending no longer recites fragments of SEQ ID NO:8; thus, the rejection of claims 3, 6, 7, under 35 U.S.C. § 102(e) has been rendered moot.

With respect to the claimed variants, the alignment for GenSeq Record No. AAZ38150 shown in the tBLASTx analysis included with this Response demonstrate that Fearon *et al.* fails to disclose either of SEQ ID NO:8 or 90% variants of SEQ ID NO:8, as recited in Claims 3 and 9; neither does Fearon *et al.* disclose any of SEQ ID NO:30 itself, 70% variants of SEQ ID NO:30, complements of either SEQ ID NO:30 or 70% variants of SEQ ID NO:30, or RNA equivalents of any of the preceding, as recited in claim 11.

Applicants therefore respectfully request that the rejection under 35 U.S.C. § 102(e) be withdrawn.

Rejection of Claims 3-7, 9 and 11 under the utility requirement of 35 U.S.C. section 101 and derivatively under the enablement requirement of 35 U.S.C. section 112, 1st paragraph

The Examiner has rejected claims 3-7, 9 and 11 under 35 U.S.C. § 101, because the claimed invention is not supported by either a specific asserted utility or a well-established utility. The rejection

alleges in particular that:

- "...the instant disclosure fails to disclose any biological functions or activities of the claimed polypeptide." (Office Action of November 4, 2002, pages 5 to 6).
- "...it would require undue experimentation for one skilled in the art to make and use the claimed genus of polynucleotides and polypeptides embraced by the instant claims." (Office Action of November 4, 2002, page 8).

Applicants traverse the rejection for at least the following reasons.

The rejection of claims 3-7, 9, and 11 is improper, as the inventions of those claims have a patentable utility as set forth in the instant specification, and/or a utility well-known to one of ordinary skill in the art.

The invention at issue is a polynucleotide (SEQ ID NO:30) corresponding to a full-length expressed signal peptide (SEQ ID NO:8) that is expressed in reproductive, hematopoietic/immune, gastrointestinal, and nervous tissues in humans, exhibits homology to human complement receptor 1 (GenBank record number g563324). See Tables 2 and 3 of the specification as originally filed. The encoded polypeptide possess the following signature sequences, motifs, and domains: a signal sequence (amino acid residues M1-Q34); sushi sequences (residues C35-C91 and C96-C153); complement factor H repeats (!34 to S95 and K88-D154) and a complement pathway membrane protein domain (M1-S95). See Table 2 of the specification. Expression of the claimed polynucleotide is associated with cancer, inflammation/trauma, and cell proliferation. See Table 3 of the specification.

The claimed invention has numerous practical, beneficial uses in toxicology testing, drug development, and the diagnosis of disease, none of which requires knowledge of how the polypeptide coded for by the polynucleotide actually functions.

In support of this assertion, applicants submit three expert Declarations under 37 C.F.R. § 1.132, with respective attachments, and ten (10) scientific references filed before or shortly after the May 14, 1999, priority date of the instant application. The Rockett Declaration, Iyer Declaration,

Bedilion Declaration, and the ten (10) references establish that, prior to the May 14, 1999 filing date of the parent application, it was well-established in the art that:

> polynucleotides derived from nucleic acids expressed in one or more tissues and/or cell types can be used as hybridization probes -- that is, as tools -- to survey for and to measure the presence, the absence, and the amount of expression of their cognate gene;
>
> with sufficient length, at sufficient hybridization stringency, and with sufficient wash stringency -- conditions that can be routinely established -- expressed polynucleotides, used as probes, generate a signal that is specific to the cognate gene, that is, produce a gene-specific expression signal;
>
> expression analysis is useful, *inter alia*, in drug discovery and lead optimization efforts, in toxicology, particularly toxicology studies conducted early in drug development efforts, and in phenotypic characterization and categorization of cell types, including neoplastic cell types;
>
> each additional gene-specific probe used as a tool in expression analysis provides an additional gene-specific signal that could not otherwise have been detected, giving a more comprehensive, robust, higher resolution, statistically more significant, and thus more useful expression pattern in such analyses than would otherwise have been possible;
>
> biologists, such as toxicologists, recognize the increased utility of more comprehensive, robust, higher resolution, statistically more significant results, and thus want each newly identified expressed gene to be included in such an analysis;
>
> nucleic acid microarrays increase the parallelism of expression measurements, providing expression data analogous to that provided by older, lower throughput techniques, but at substantially increased throughput;
>
> accordingly, when expression profiling is performed using microarrays, each additional gene-specific probe that is included as a signaling component on this analytical device increases the detection range, and thus versatility, of this research tool;

biologists, such as toxicologists, recognize the increased utility of such improved tools, and thus want a gene-specific probe to each newly identified expressed gene to be included in such an analytical device;

the industrial suppliers of microarrays recognize the increased utility of such improved tools to their customers, and thus strive to improve salability of their microarrays by adding each newly identified expressed gene to the microarrays they sell;

it is not necessary that the biological function of a gene be known for measurement of its expression to be useful in drug discovery and lead optimization analyses, toxicology, or molecular phenotyping experiments;

failure of a probe to detect changes in expression of its cognate gene does not diminish the usefulness of the probe as a research tool; and

failure of a probe completely to detect its cognate transcript in any single expression analysis experiment does not deprive the probe of usefulness to the community of users who would use it as a research tool.

The Patent Examiner does not dispute that the claimed polynucleotide can be used as a probe in cDNA microarrays and used in gene expression monitoring applications. Instead, the Patent Examiner contends that the claimed polynucleotide cannot be useful without precise knowledge of its biological function, or the biological function of the polypeptide it encodes. But the law has never required knowledge of biological function to prove utility. It is the claimed invention's uses, not its functions, that are the subject of a proper analysis under the utility requirement.

In any event, as demonstrated by the the Rockett Declaration, the Iyer Declaration, and the Bedilion Declaration, the person of ordinary skill in the art can achieve beneficial results from the claimed polynucleotide in the absence of any knowledge as to the precise function of the protein encoded by it. The uses of the claimed polynucleotide in gene expression monitoring applications are in fact independent of its precise biological function.

Enablement Rejection under 35 U.S.C. section 112, first paragraph

This rejection is based in part on the assertions already discussed above, *i.e.*, that the claimed invention lacks patentable utility. See the Office Action of November 4th, 2002. To the extent that the rejection under § 112, first paragraph, is based on improper allegation of lack of patentable utility under § 101, it fails for the same reasons.

In addition, Claims 3, 6, 7 and 9 were rejected under 35 U.S.C. § 112, first paragraph, based on the allegation that the specification does not describe the subject matter of the invention in such a way as to enable one of skill in the art to make and/or use the claimed polynucleotide fragments. In particular, the Office Action asserts that "...the disclosure fails to provide sufficient guidance, information or working examples regarding the structural and functional requirements commensurate in scope with what is encompassed by the instant claims." See page 7 of the Office Action of November 4, 2002.

As a preliminary matter, the claims have been amended to delete the "fragment" language, thereby rendering the rejection moot to the extent it was applicable to this part of the rejection.

By these amendments, Applicants expressly do not disclaim equivalents of the claimed invention. Applicants do not concede to the Patent Office position; Applicants are amending the claims solely to obtain expeditious allowance of the instant application.

Moreover, Applicants disagree with the Examiner's basic premise, that because the relationship between protein sequence, its consequent tertiary structure, and its resulting function is not well understood and therefore unpredictable, that the claimed invention of 90% variants of SEQ ID NO:8 is not sufficiently enabled.

The Examiner misunderstands the nature of the requisite enablement in the present case. With respect to polynucleotides encoding 90% variants of SEQ ID NO:8, one desiring to make applicant's invention need not decide *a priori* what modifications need be made to SEQ ID NO:8. Instead, he or she need only possess the very ordinary skills required to make or isolate a polynucleotide encoding a *naturally occurring* amino acid sequence having 90% sequence identity to SEQ ID NO:8. In other

words, nature itself will have, through natural selection, already determined the sequence of the claimed variants. Thus the scope of the claimed invention is, with respect to the claimed variants, considerably narrower than the Examiner suggests.

For at least these reasons, withdrawal of the enablement rejection is requested..

Rejection of Claims 3, 6, 7, 9 and 11 under the written description requirement of 35 U.S.C. § 112, 1st paragraph

Claims 3, 6, 7, 9 and 11 have been rejected pursuant to 35 U.S.C. section 112, first paragraph for alleged lack of written description, for the reason that they "contain[] subject matter which as not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor, at the time the application was filed, had possession of the claimed invention. In particular, the Examiner alleges that, with respect to the claimed polynucleotides encoding 90% sequence variants of SEQ ID NO:8, and the 70% polynucleotide sequence variants of SEQ ID NO:30, "...the claims encompass a huge number of nucleic acids that vary substantially both in length and in nucleotide composition.

With respect to polynucleotides encoding polypeptide fragments of SEQ ID NO:8, claim 3 has been amended such that these molecules are no longer recited. By these amendments, Applicants expressly do not disclaim equivalents of the claimed invention. Applicants do not concede to the Patent Office position; Applicants are amending the claim solely to obtain expeditious allowance of the instant application.

With respect to the claimed polypeptide and polynucleotide variants, Applicants traverse the rejection for at least the following reasons.

The requirements necessary to fulfill the written description requirement of 35 U.S.C. 112, first paragraph, are well established by case law.

> . . . the applicant must also convey with reasonable clarity to those skilled in the art that, as of the filing date sought, he or she was in possession *of the invention.*

> The invention is, for purposes of the "written description" inquiry, *whatever is now claimed. Vas-Cath, Inc. v. Mahurkar*, 19 USPQ2d 1111, 1117 (Fed. Cir. 1991).

Attention is drawn to the Patent and Trademark Office's own "Guidelines for Examination of Patent Applications Under the 35 U.S.C. Sec. 112, para. 1", published January 5, 2001, which provide that :

> An applicant may also show that an invention is complete by disclosure of sufficiently detailed, relevant identifying characteristics which provide evidence that applicant was in possession of the claimed invention, i.e., complete or partial structure, other physical and/or chemical properties, functional characteristics when coupled with a known or disclosed correlation between function and structure, or some combination of such characteristics. What is conventional or well known to one of ordinary skill in the art need not be disclosed in detail. If a skilled artisan would have understood the inventor to be in possession of the claimed invention at the time of filing, even if every nuance of the claims is not explicitly described in the specification, then the adequate description requirement is met. (footnotes omitted.)

Thus, the written description standard is fulfilled by both what is specifically disclosed and what is conventional or well known to one skilled in the art.

I. The specification provides an adequate written description of the recited "variants" of SEQ ID NO:8

The subject matter encompassed by claims 3, 6, 7, 9 and 11 is either disclosed by the Specification or is conventional or well known to one skilled in the art.

First note that the "variant" language of independent Claim 3 recites an isolated polynucleotide encoding "an isolated polypeptide comprising ... a naturally occurring amino acid sequence having at least 90% sequence identity to the amino acid sequence of SEQ ID NO:8," and the "variant" language of independent claim 11 recites "a polynucleotide comprising a naturally occurring polynucleotide sequence having at least 90% sequence identity to the polynucleotide sequence of SEQ ID NO:30."

The amino acid sequence of SEQ ID NO:8 and the polynucleotide sequence of SEQ ID NO:30 are explicitly disclosed in the specification. See, for example, the Sequence Listing. Similarly,

variants of SEQ ID NO:8 and SEQ ID NO:30 are described in the Specification at, for example, page 12, lines 16-31; and page 23, line 35 to page 24, line 21

One of ordinary skill in the art would recognize polynucleotide sequences which are variants having a polynucleotide sequence at least 90% identical to SEQ ID NO:30, or which encode polypeptide variants having an amino acid sequence at least 90% identical to SEQ ID NO:8. Given any naturally occurring polynucleotide sequence, it would be routine for one of skill in the art to recognize whether it was a variant of SEQ ID NO:30, or whether it encoded a variant of SEQ ID NO:8. Accordingly, the specification provides an adequate written description of the recited polynucleotide variants of SEQ ID NO:30 and polynucleotides encoding polypeptide variants of SEQ ID NO:8.

There simply is no requirement that the claims recite particular amino acid "variant" sequences because, as discussed above, the Specification already provides sufficient structural definition of the claimed subject matter. Because the recited amino acid "variants" are defined in terms of SEQ ID NO:8, the precise chemical structure of every amino acid variant within the scope of the claims can be discerned. Accordingly, the Specification provides an adequate written description of the claimed sequences. The Examiner's position is nothing more than a misguided attempt to require Appellants to unduly limit the scope of their claimed invention.

1. The present claim specifically defines the claimed genus through the recitation of chemical structure

Court cases in which "DNA claims" have been at issue commonly emphasize that the recitation of structural features or chemical or physical properties are important factors to consider in a written description analysis of such claims. For example, in *Fiers v. Revel*, 25 USPQ2d 1601, 1606 (Fed. Cir. 1993), the court stated that:

> If a conception of a DNA requires a precise definition, such as by structure, formula, chemical name or physical properties, as we have held, then a description also requires that degree of specificity.

In a number of instances in which claims to DNA have been found invalid, the courts have noted that the claims attempted to define the claimed DNA in terms of functional characteristics without any reference to structural features. As set forth by the court in *University of California v. Eli Lilly and Co.*, 43 USPQ2d 1398, 1406 (Fed. Cir. 1997):

> In claims to genetic material, however, a generic statement such as "vertebrate insulin cDNA" or "mammalian insulin cDNA," without more, is not an adequate written description of the genus because it does not distinguish the claimed genus from others, except by function.

Thus, the mere recitation of functional characteristics of a DNA, without the definition of structural features, has been a common basis by which courts have found invalid claims to DNA. For example, in *Lilly*, 43 USPQ2d at 1407, the court found invalid for violation of the written description requirement the following claim of U.S. Patent No. 4,652,525:

> 1. A recombinant plasmid replicable in procaryotic host containing within its nucleotide sequence a subsequence having the structure of the reverse transcript of an mRNA of a vertebrate, which mRNA encodes insulin.

In *Fiers*, 25 USPQ2d at 1603, the parties were in an interference involving the following count:

> A DNA which consists essentially of a DNA which codes for a human fibroblast interferon-beta polypeptide.

Party Revel in the *Fiers* case argued that its foreign priority application contained an adequate written description of the DNA of the count because that application mentioned a potential method for isolating the DNA. The Revel priority application, however, did not have a description of any particular DNA structure corresponding to the DNA of the count. The court therefore found that the Revel priority application lacked an adequate written description of the subject matter of the count.

Thus, in *Lilly* and *Fiers*, nucleic acids were defined on the basis of functional characteristics and were found not to comply with the written description requirement of 35 U.S.C. §112; *i.e.*, "an

mRNA of a vertebrate, which mRNA encodes insulin" in *Lilly*, and "DNA which codes for a human fibroblast interferon-beta polypeptide" in *Fiers*.

In contrast to the situation in *Lilly* and *Fiers*, the claims at issue in the present application define polynucleotides which code polypeptides in terms of chemical structure, rather than functional characteristics. For example, the "variant" language of independent Claim 3 and Claim 11 recites chemical structure to define the claimed genus:

Claim 3:

3. An isolated polynucleotide encoding an isolated polypeptide comprising an amino acid sequence selected from the group consisting of:

a) the amino acid sequence of SEQ ID NO:8, and

a) a naturally occurring amino acid sequence having at least 90% sequence identity to the amino acid sequence of SEQ ID NO:8.

Claim 11:

11. An isolated polynucleotide comprising a polynucleotide sequence selected from the group consisting of:

a) a polynucleotide sequence comprising SEQ ID NO:30,

b) a naturally occurring polynucleotide sequence having at least 70% sequence identity to a polynucleotide sequence comprising SEQ ID NO:30,

c) a polynucleotide sequence complementary to a),

d) a polynucleotide sequence complementary to b), and

e) an RNA equivalent of a)-d).

From the above it should be apparent that the claims of the subject application are fundamentally different from those found invalid in *Lilly* and *Fiers*. The subject matter of the present claims is defined in terms of the chemical structure of SEQ ID NO:8 and SEQ ID NO:30. In the present case, there is no reliance merely on a description of functional characteristics of the

polypeptides which are encoded by the polynucleotides. The polynucleotides and polypeptides defined in the claims of the present application recite structural features, and cases such as *Lilly* and *Fiers* stress that the recitation of structure is an important factor to consider in a written description analysis of claims of this type. By failing to base its written description inquiry "on whatever is now claimed," the Office Action failed to provide an appropriate analysis of the present claims and how they differ from those found not to satisfy the written description requirement in *Lilly* and *Fiers*.

Further, consider the case of *Amgen Inc. v. Chugai Pharmaceutical Co. Ltd.*, 18 USPQ2d 1016(Fed. Cir. 1991). In that case, the independent claim at issue reads as follows:

> 7. A purified and isolated DNA sequence consisting essentially of a DNA sequence encoding a polypeptide having an amino acid sequence sufficiently duplicative of that of erythropoietin to allow possession of the biological property of causing bone marrow cells to increase production of reticulocytes and red blood cells, and to increase hemoglobin synthesis or iron uptake.

As stated by the court at page 1026 in *Amgen*:

> Claim 7 is a generic claim, **covering all possible DNA sequences that will encode any polypeptide** having an amino acid sequence "sufficiently duplicative" of EPO to possess the property of increasing production of red blood cells. (emphasis added)

In addition, from the discussion at pages 1026-1027 it is apparent that the patentee of claim 7 in *Amgen* had engaged in making man-made analogs of erythropoietin. Thus, the subject matter defined by claim 7 in the *Amgen* case had no limitation as to whether the DNA sequences of the erythropoietin molecules were naturally-occurring or man-made.

This is a situation far removed from the subject matter defined by the claims on appeal here, where the claims recite polynucleotides encoding polypeptides comprising a **naturally occurring amino acid sequence** having at least 90% sequence identity to the amino acid sequence of SEQ ID NO:8." As discussed at above, the present Specification describes how to make polynucleotides encoding the claimed variants of SEQ ID NO:8 which comprise naturally-occurring sequences.

2. The present claims do not define a genus which is "highly variant"

Furthermore, the claims at issue do not describe a genus which could be characterized as "highly variant". Available evidence illustrates that, rather than being a large variable genus, the claimed genus is of narrow scope.

In support of this assertion, the Examiner's attention is directed to the enclosed reference by Brenner et al. (Assessing sequence comparison methods with reliable structurally identified distant evolutionary relationships, Proc. Natl. Acad. Sci. USA (1998) 95:6073-6078). Through exhaustive analysis of a data set of proteins with known structural and functional relationships and with <90% overall sequence identity, Brenner et al. have determined that 30% identity is a reliable threshold for establishing evolutionary homology between two sequences aligned over at least 150 residues. (Brenner et al., pages 6073 and 6076.) Furthermore, local identity is particularly important in this case for assessing the significance of the alignments, as Brenner et al. further report that ≥40% identity over at least 70 residues is reliable in signifying homology between proteins. (Brenner et al., page 6076.)

The present application is directed, *inter alia*, to polynucleotides which encode polypeptides related to the amino acid sequence of SEQ ID NO:8. In accordance with Brenner et al., naturally occurring molecules may exist which could be characterized as full-length expressed genetic markers and which have as little as 30% identity over at least 150 residues to SEQ ID NO:8. The "variant language"of the present claims recites, for example, a polypeptide comprising "a naturally occurring amino acid sequence at least 90% identical to the amino acid sequence of SEQ ID NO:8." This variation is far less than that of all potential full-length expressed genetic markers related to SEQ ID NO:8, i.e., those full-length expressed genetic markers having as little as 30% identity over at least 150 residues to SEQ ID NO:8.

3. The state of the art at the time of the present invention is further advanced than at the time of the *Lilly* and *Fiers* applications

In the *Lilly* case, claims of U.S. Patent No. 4,652,525 were found invalid for failing to comply with the written description requirement of 35 U.S.C. §112. The '525 patent claimed the benefit of priority of two applications, Application Serial No. 801,343 filed May 27, 1977, and Application Serial No. 805,023 filed June 9, 1977. In the *Fiers* case, party Revel claimed the benefit of priority of an Israeli application filed on November 21, 1979. Thus, the written description inquiry in those case was based on the state of the art at essentially at the "dark ages" of recombinant DNA technology.

The present application has a priority date of July 21, 1999. Much has happened in the development of recombinant DNA technology in the 20 or so years from the time of filing of the applications involved in *Lilly* and *Fiers* and the present application. For example, the technique of polymerase chain reaction (PCR) was invented. Highly efficient cloning and DNA sequencing technology has been developed. Large databases of protein and nucleotide sequences have been compiled. Much of the raw material of the human and other genomes has been sequenced. With these remarkable advances one of skill in the art would recognize that, given the sequence information of SEQ ID NO:8 and SEQ ID NO:30, and the additional extensive detail provided by the subject application, the present inventors were in possession of the claimed polypeptide variants at the time of filing of this application.

4. Summary

The Office Action failed to base its written description inquiry "on whatever is now claimed." Consequently, the Action did not provide an appropriate analysis of the present claims and how they differ from those found not to satisfy the written description requirement in cases such as *Lilly*, *Fiers,* and *Amgen*. In particular, the claims of the subject application are fundamentally different from those found invalid in *Lilly*, *Fiers,* and *Amgen*. The subject matter of the present claims is defined in terms of the chemical structure of SEQ ID NO:8 and SEQ ID NO:30. The courts have stressed that structural features are important factors to consider in a written description analysis of claims to nucleic acids and proteins. In addition, the genus of polynucleotides which encode the polypeptides defined by the present claims is adequately described, as evidenced by Brenner et al. Furthermore, there have been

remarkable advances in the state of the art since the *Lilly* and *Fiers* cases, and these advances were given no consideration whatsoever in the position set forth by the Office Action.

For at least the above reasons, withdrawal of this rejection is requested.

CONCLUSION

In light of the above amendments and remarks, Applicants submit that the present application is fully in condition for allowance, and request that the Examiner withdraw the outstanding rejections. Early notice to that effect is earnestly solicited.

If the Examiner contemplates other action, or if a telephone conference would expedite allowance of the claims, Applicants invite the Examiner to contact Applicants' Attorney at (650) 855-0555.

The Applicants believe that no fee is due with this communication. However, if the Commissioner determines that additional fees are due or that an excess fee has been paid, the Patent Office is authorized to debit or credit (respectively) Deposit Account No. **09-0108**.

Respectfully submitted,
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Date: 10 March 2004

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Program: tblastn
Sequence ID(s):
seqidno:8_103561CB1 vs. Current.Geneseq.NA.fasta

NCBI-TBLASTN 2.0.10 [Aug-26-1999]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= seqidno:8_103561CB1
(174 letters)

Database: Current.Geneseq.NA.fasta
3,532,328 sequences; 2,242,417,501 total letters

Searching.....done

Sequences producing significant alignments:		Score (bits)	E Value
GSEQ:ABQ99306	Human coding sequence SEQ ID 39.	372	e-102
GSEQ:AAF58602	Human RECAP polynucleotide, SEQ ID NO: 30.	372	e-102
GSEQ:ABX34686	Human mddt cDNA SEQ ID 247.	256	5e-67
GSEQ:AAS64474	DNA encoding novel human diagnostic protein #27	256	5e-67
GSEQ:ADE85074	Farnesyl transferase inhibitor modulated leukem	256	5e-67
GSEQ:ABA91636	Human C3B/C4B receptor CR1 (complement receptor	256	5e-67
GSEQ:ABK84738	Human cDNA differentially expressed in granuloc	256	5e-67
GSEQ:AAZ38150	Human C3b/C4b receptor (CR1) protein encoding D	256	5e-67
GSEQ:AAQ11642	Entire human complement type 1 receptor coding	256	5e-67
GSEQ:AAN91477	CR1 protein DNA.	256	5e-67

>GSEQ:ABQ99306 Human coding sequence SEQ ID 39.
Length = 677

Score = 372 bits (946), Expect = e-102
Identities = 174/174 (100%), Positives = 174/174 (100%)
Frame = +2

Query: 1 MAPPVRLERPFPSRRFPGLLLAALVLLLSSFSDQCNVPEWLPFARPTNLTDDFEFPIGTY 60

```
 Score = 37.5 bits (85), Expect = 0.40
 Identities = 33/117 (28%), Positives = 51/117 (43%), Gaps = 21/117 (17%)
 Frame = +1

Query: 37   VPEWLPFARPTNLTDDF------EFPIGTYLNYECRPGYSGRPF-------SIICLKN-- 81
            +P  LP   PT    DF       F  G+ + Y C PG  GR         SI C  N
Sbjct: 1867 IPCGLP---PTIANGDFISTNRENFHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDD 2037

Query: 82   --SVWTSAKDKCKRKSCRNPPDPVNGMAHVIKD----IQFGSQIKYSCPKGYRLIGSSSA 135
               +W+    +C   +   PP+  NG+  ++ D          +++ C  G+ + G
Sbjct: 2038 QVGIWSGPAPQCIIPNKCTPPNVENGI--LVSDNRSLFSLNEVVEFRCQPGFVMKGPRRV 2211

Query: 136  TCIISGNTVIWDNKTPVC 153
              C       W+ + P C
Sbjct: 2212 KCQALNK---WEPELPSC 2256


 Score = 37.5 bits (85), Expect = 0.40
 Identities = 33/117 (28%), Positives = 51/117 (43%), Gaps = 21/117 (17%)
 Frame = +1

Query: 37  VPEWLPFARPTNLTDDF------EFPIGTYLNYECRPGYSGRPF-------SIICLKN-- 81
           +P  LP   PT    DF       F  G+ + Y C PG  GR         SI C  N
Sbjct: 517 IPCGLP---PTITNGDFISTNRENFHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDD 687

Query: 82  --SVWTSAKDKCKRKSCRNPPDPVNGMAHVIKD----IQFGSQIKYSCPKGYRLIGSSSA 135
              +W+    +C   +   PP+  NG+  ++ D          +++ C  G+ + G
Sbjct: 688 QVGIWSGPAPQCIIPNKCTPPNVENGI--LVSDNRSLFSLNEVVEFRCQPGFVMKGPRRV 861

Query: 136 TCIISGNTVIWDNKTPVC 153
             C       W+ + P C
Sbjct: 862 KCQALNK---WEPELPSC 906


>GSEQ:AAZ38150 Human C3b/C4b receptor (CR1) protein encoding DNA.
          Length = 6951

 Score =  256 bits (647), Expect = 5e-67
 Identities = 117/137 (85%), Positives = 125/137 (90%), Gaps = 1/137 (0%)
 Frame = +1

Query: 18  GLLLAALVLLLSSFS-DQCNVPEWLPFARPTNLTDDFEFPIGTYLNYECRPGYSGRPFSI 76
           G LLA +VLL    +  QCN PEWLPFARPTNLTD+FEFPIGTYLNYECRPGYSGRPFSI
Sbjct: 100 GSLLAVVVLLALPVAWGQCNAPEWLPFARPTNLTDEFEFPIGTYLNYECRPGYSGRPFSI 279

Query: 77  ICLKNSVWTSAKDKCKRKSCRNPPDPVNGMAHVIKDIQFGSQIKYSCPKGYRLIGSSSAT 136
           ICLKNSVWT AKD+C+RKSCRNPPDPVNGM HVIK IQFGSQIKYSC KGYRLIGSSSAT
Sbjct: 280 ICLKNSVWTGAKDRCRRKSCRNPPDPVNGMVHVIKGIQFGSQIKYSCTKGYRLIGSSSAT 459

Query: 137 CIISGNTVIWDNKTPVCD 154
           CIISG+TVIWDN+TP+CD
Sbjct: 460 CIISGDTVIWDNETPICD 513


 Score =  176 bits (442), Expect = 5e-43
 Identities = 75/127 (59%), Positives = 92/127 (72%)
 Frame = +1

Query: 28   LSSFSDQCNVPEWLPFARPTNLTDDFEFPIGTYLNYECRPGYSGRPFSIICLKNSVWTSA 87
           LS  +  C   PE   PFA PT    +DFEFP+GT LNYECRPGY G+ FSI CL+N VW+S
Sbjct: 4192 LSVRAGHCKTPEQFPFASPTIPINDFEFPVGTSLNYECRPGYFGKMFSISCLENLVWSSV 4371

Query: 88   KDKCKRKSCRNPPDPVNGMAHVIKDIQFGSQIKYSCPKGYRLIGSSSATCIISGNTVIWD 147
           +D C+RKSC  PP+P NGM H+  D QFGS + YSC +G+RLIGS S TC++SGN V WD
Sbjct: 4372 EDNCRRKSCGPPPEPFNGMVHINTDTQFGSTVNYSCNEGFRLIGSPSTTCLVSGNNVTWD 4551
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Query: 148  NKTPVCD 154
             K P+C+
Sbjct: 4552 KKAPICE 4572


 Score =  166 bits (417), Expect = 5e-40
 Identities = 75/119 (63%), Positives = 85/119 (71%)
 Frame = +1

Query: 35   CNVPEWLPFARPTNLTDDFEFPIGTYLNYECRPGYSGRPFSIICLKNSVWTSAKDKCKRK 94
             C  P+   FA+    T+  +FPIGT L YECRP Y GRPFSI CL N VW+S KD CKRK
Sbjct: 2854 CQAPDHFLFAKLKTQTNASDFPIGTSLKYECRPEYYGRPFSITCLDNLVWSSPKDVCKRK 3033

Query: 95   SCRNPPDPVNGMAHVIKDIQFGSQIKYSCPKGYRLIGSSSATCIISGNTVIWDNKTPVC 153
             SC+ PPDPVNGM HVI DIQ GS+I YSC  G+RLIG SSA CI+SGNT  W  K P+C
Sbjct: 3034 SCKTPPDPVNGMVHVITDIQVGSRINYSCTTGHRLIGHSSAECILSGNTAHWSTKPPIC 3210


 Score =  164 bits (412), Expect = 2e-39
 Identities = 74/119 (62%), Positives = 84/119 (70%)
 Frame = +1

Query: 35   CNVPEWLPFARPTNLTDDFEFPIGTYLNYECRPGYSGRPFSIICLKNSVWTSAKDKCKRK 94
             C  P+   FA+    T+  +FPIGT L YECRP Y GRPFSI CL N VW+S KD CKRK
Sbjct: 1504 CQAPDHFLFAKLKTQTNASDFPIGTSLKYECRPEYYGRPFSITCLDNLVWSSPKDVCKRK 1683

Query: 95   SCRNPPDPVNGMAHVIKDIQFGSQIKYSCPKGYRLIGSSSATCIISGNTVIWDNKTPVC 153
             SC+ PPDPVNGM HVI DIQ GS+I YSC  G+RLIG SSA CI+SGN   W  K P+C
Sbjct: 1684 SCKTPPDPVNGMVHVITDIQVGSRINYSCTTGHRLIGHSSAECILSGNAAHWSTKPPIC 1860


 Score = 68.7 bits (165), Expect = 2e-10
 Identities = 40/127 (31%), Positives = 65/127 (50%), Gaps = 2/127 (1%)
 Frame = +1

Query: 28   LSSFSDQCNVPEWLPFARPTNLTDDFEFPIGTYLNYECRPGYSGR-PFSIICLKNSVWTS 86
             L S S  C  P  +  A  T    D  F  G  + Y C PGY  R   S+ C     W+
Sbjct: 2245 LPSCSRVCQPPPDVLHAERTQRDKD-NFSPGQEVFYSCEPGYDLRGAASMRCTPQGDWSP 2421

Query: 87   AKDKCKRKSCRN-PPDPVNGMAHVIKDIQFGSQIKYSCPKGYRLIGSSSATCIISGNTVI 145
             A   C+ KSC +     +NG      ++Q G+++ + C +G++L GSS++ C++G   +
Sbjct: 2422 AAPTCEVKSCDDFMGQLLNGRVLFPVNLQLGAKVDFVCDEGFQLKGSSASYCVLAGMESL 2601

Query: 146  WDNKTPVCD 154
             W++  PVC+
Sbjct: 2602 WNSSVPVCE 2628


 Score = 68.7 bits (165), Expect = 2e-10
 Identities = 40/127 (31%), Positives = 65/127 (50%), Gaps = 2/127 (1%)
 Frame = +1

Query: 28   LSSFSDQCNVPEWLPFARPTNLTDDFEFPIGTYLNYECRPGYSGR-PFSIICLKNSVWTS 86
             L S S  C  P  +  A  T    D  F  G  + Y C PGY  R   S+ C     W+
Sbjct: 895  LPSCSRVCQPPPDVLHAERTQRDKD-NFSPGQEVFYSCEPGYDLRGAASMRCTPQGDWSP 1071

Query: 87   AKDKCKRKSCRN-PPDPVNGMAHVIKDIQFGSQIKYSCPKGYRLIGSSSATCIISGNTVI 145
             A   C+ KSC +     +NG      ++Q G+++ + C +G++L GSS++ C++G   +
Sbjct: 1072 AAPTCEVKSCDDFMGQLLNGRVLFPVNLQLGAKVDFVCDEGFQLKGSSASYCVLAGMESL 1251

Query: 146  WDNKTPVCD 154
             W++  PVC+
Sbjct: 1252 WNSSVPVCE 1278


 Score = 64.8 bits (155), Expect = 2e-09
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```
 Identities = 39/127 (30%), Positives = 61/127 (47%), Gaps = 2/127 (1%)
 Frame = +1

Query: 28   LSSFSDQCNVPEWLPFARPTNLTDDFEFPIGTYLNYECRPGYSGR-PFSIICLKNSVWTS 86
            L S S  C  P  +      T    D  F  G  + Y  C PGY  R   S+ C     W+
Sbjct: 3595 LPSCSRVCQPPPEILHGEHTPSHQD-NFSPGQEVFYSCEPGYDLRGAASLHCTPQGDWSP 3771

Query: 87   AKDKCKRKSCRNPPDPV-NGMAHVIKDIQFGSQIKYSCPKGYRLIGSSSATCIISGNTVI 145
               +C  KSC +     + +G       ++Q G+++ + C +G+RL GSS + C++ G   +
Sbjct: 3772 EAPRCAVKSCDDFLGQLPHGRVLFPLNLQLGAKVSFVCDEGFRLKGSSVSHCVLVGMRSL 3951

Query: 146  WDNKTPVCD 154
            W+N  PVC+
Sbjct: 3952 WNNSVPVCE 3978


 Score = 61.3 bits (146), Expect = 3e-08
 Identities = 30/106 (28%), Positives = 56/106 (52%), Gaps = 2/106 (1%)
 Frame = +1

Query: 49   LTDDFEFPIGTYLNYECRPGYSGR-PFSIICLKNSVWTSAKDKCKRKSCRNPPDPV-NGM 106
            L+    F  G  + Y C P Y  R   S+ C     W+    +C  KSC +     + +G
Sbjct: 5014 LSHQDNFSPGQEVFYSCEPSYDLRGAASLHCTPQGDWSPEAPRCTVKSCDDFLGQLPHGR 5193

Query: 107  AHVIKDIQFGSQIKYSCPKGYRLIGSSSATCIISGNTVIWDNKTPVCD 154
              +  ++Q G+++ + C +G+RL G S++ C+++G   +W++  PVC+
Sbjct: 5194 VLLPLNLQLGAKVSFVCDEGFRLKGRSASHCVLAGMKALWNSSVPVCE 5337


 Score = 48.0 bits (112), Expect = 3e-04
 Identities = 44/133 (33%), Positives = 60/133 (45%), Gaps = 18/133 (13%)
 Frame = +1

Query: 26   LLLSSFSDQCNV----PEWLPFARPTNLTDDFEFPIGTYLNYECRPGYS--GRPFSIICL 79
            L+ SS  D C      P   PF    ++  D +F  G+ +NY C  G+   G P S  CL
Sbjct: 4354 LVWSSVEDNCRRKSCGPPPEPFNGMVHINTDTQF--GSTVNYSCNEGFRLIGSP-STTCL 4524

Query: 80   ---KNSVWTSAKDKCKRKSCRNPPDPVNGMAHVIKDIQF--GSQIKYSCPKG------YR 128
               N  W      C+  SC  PP   NG  +      F  G+ + Y C  G      +
Sbjct: 4525 VSGNNVTWDKKAPICEIISCEPPPTISNGDFYSNNRTSFHNGTVVTYQCHTGPDGEQLFE 4704

Query: 129  LIGSSSATCIISGNTV-IWDNKTPVCDSELK 158
            L+G  S  C    + V +W +  P C S  K
Sbjct: 4705 LVGERSIYCTSKDDQVGVWSSPPPRCISTNK 4797


 Score = 46.5 bits (108), Expect = 8e-04
 Identities = 33/98 (33%), Positives = 52/98 (52%), Gaps = 14/98 (14%)
 Frame = +1

Query: 57   IGTYLNYECRPGY--SGRPFS--IICLKNSVWTSAKDKCKRKSCRNPPDPVNG--MAHVI 110
            +G  +++ C  G+   GR  S  ++    ++W S+   C++  C NPP  +NG
Sbjct: 5218 LGAKVSFVCDEGFRLKGRSASHCVLAGMKALWNSSVPVCEQIFCPNPPAILNGRHTGTPF 5397

Query: 111  KDIQFGSQIKYSCP------KGYRLIGSSSATCII--SGNTVIWDNKTPVCD 154
             DI +G +I Y+C          + LIG SS  C     GN V W +  P C+
Sbjct: 5398 GDIPYGKEISYACDTHPDRGMTFNLIGESSIRCTSDPQGNGV-WSSPAPRCE 5550


 Score = 43.8 bits (101), Expect = 0.005
 Identities = 31/105 (29%), Positives = 45/105 (42%), Gaps = 5/105 (4%)
 Frame = +1

Query: 58   GTYLNYECRPGYS--GRPFSIICLKNSVWTSAKDKCKRKSCRNPPDPVNGMAHVI---KD 112
            G  ++Y C PGY   G+ F I C    +W+     CK  +C  P   +NG++  +   K
Sbjct: 5635 GMTISYTCDPGYLLVGKGF-IFCTDQGIWSQLDHYCKEVNCSFPLF-MNGISKELEMKKV 5808
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Query: 113  IQFGSQIKYSCPKGYRLIGSSSATCIISGNTVIWDNKTPVCDSELKYAFL 162
             +G  +    C  GY L GS  + C          WD     C S    A +
Sbjct: 5809 YHYGDYVTLKCEDGYTLEGSPWSQCQADDR---WDPPLAKCTSRAHDALI 5949


 Score = 43.8 bits (101), Expect = 0.005
 Identities = 30/96 (31%), Positives = 44/96 (45%), Gaps = 13/96 (13%)
 Frame = +1

Query: 58  GTYLNYECRPGY----SGRPFSIICLKNSVWTSAKDKCKRKSCRNPPDPVNG--MAHVIK 111
            G+ + Y C  GY    S      II      +W +    C R  C  PP   NG  ++    +
Sbjct: 397 GSQIKYSCTKGYRLIGSSSATCIISGDTVIWDNETPICDRIPCGLPPTITNGDFISTNRE 576

Query: 112 DIQFGSQIKYSCPKG------YRLIGSSSATCIISGNTV-IWDNKTPVC 153
            +  +GS + Y C  G       + L+G  S  C  + + V IW    P C
Sbjct: 577 NFHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQC 723


 Score = 43.0 bits (99), Expect = 0.009
 Identities = 29/100 (29%), Positives = 49/100 (49%), Gaps = 13/100 (13%)
 Frame = +1

Query: 54   EFPIGTYLNYECRPGYS--GRPFSIICLKNSV--WTSAKDKCKRKSCRNPPDPVNG--MA 107
             +  +G+ +NY C  G+    G    +    L  +    W++     C+R  C  PP   NG  ++
Sbjct: 1735 DIQVGSRINYSCTTGHRLIGHSSAECILSGNAAHWSTKPPICQRIPCGLPPTIANGDFIS 1914

Query: 108  HVIKDIQFGSQIKYSCPKG------YRLIGSSSATCIISGNTV-IWDNKTPVC 153
               ++   +GS + Y C  G       + L+G  S  C  + + V IW    P C
Sbjct: 1915 TNRENFHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQC 2073


 Score = 43.0 bits (99), Expect = 0.009
 Identities = 30/102 (29%), Positives = 51/102 (49%), Gaps = 14/102 (13%)
 Frame = +1

Query: 57   IGTYLNYECRPGY----SGRPFSIICLKNSVWTSAKDKCKRKSCRNPPDPVNG--MAHVI 110
             +G  +++ C  G+    S       ++      S+W ++    C+     C NPP  +NG
Sbjct: 3859 LGAKVSFVCDEGFRLKGSSVSHCVLVGMRSLWNNSVPVCEHIFCPNPPAILNGRHTGTPS 4038

Query: 111  KDIQFGSQIKYSCP------KGYRLIGSSSATCIIS--GNTVIWDNKTPVCDSELK 158
              DI +G +I Y+C             + LIG S+  C      GN V W +  P C+  ++
Sbjct: 4039 GDIPYGKEISYTCDPHPDRGMTFNLIGESTIRCTSDPHGNGV-WSSPAPRCELSVR 4203


 Score = 42.6 bits (98), Expect = 0.012
 Identities = 29/100 (29%), Positives = 49/100 (49%), Gaps = 13/100 (13%)
 Frame = +1

Query: 54   EFPIGTYLNYECRPGYSGRPFS----IICLKNSVWTSAKDKCKRKSCRNPPDPVNG--MA 107
             +  +G+ +NY C  G+       S    I+     + W++     C+R  C  PP   NG  ++
Sbjct: 3085 DIQVGSRINYSCTTGHRLIGHSSAECILSGNTAHWSTKPPICQRIPCGLPPTIANGDFIS 3264

Query: 108  HVIKDIQFGSQIKYSCPKG------YRLIGSSSATCIISGNTV-IWDNKTPVC 153
               ++   +GS + Y C  G       + L+G. S  C  + + V IW    P C
Sbjct: 3265 TNRENFHYGSVVTYRCNLGSRGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQC 3423


 Score = 41.4 bits (95), Expect = 0.027
 Identities = 30/97 (30%), Positives = 50/97 (50%), Gaps = 15/97 (15%)
 Frame = +1

Query: 57   IGTYLNYECRPGY----SGRPFSIICLKNSVWTSAKDKCKRKSCRNPPDPVNGMAHVIKD 112
             +G  +++ C  G+    S    + ++      S+W S+    C++    C  +PP   NG  H  K
Sbjct: 1159 LGAKVDFVCDEGFQLKGSSASYCVLAGMESLWNSSVPVCEQIFCPSPPVIPNG-RHTGKP 1335

Query: 113  IQ---FGSQIKYSCP------KGYRLIGSSSATCII--SGNTVIWDNKTPVC 153
             ++    FG   + Y+C            + LIG  S+  C      GN  V W +  P C
```

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Sbjct: 1336 LEVFPFGKAVNYTCDPHPDRGTSFDLIGESTIRCTSDPQGNGV-WSSPAPRC 1488


 Score = 41.4 bits (95), Expect = 0.027
 Identities = 30/97 (30%), Positives = 50/97 (50%), Gaps = 15/97 (15%)
 Frame = +1

Query: 57   IGTYLNYECRPGY----SGRPFSIICLKNSVWTSAKDKCKRKSCRNPPDPVNGMAHVIKD 112
            +G  +++ C  G+    S   + ++    S+W S+   C++  C +PP   NG  H  K
Sbjct: 2509 LGAKVDFVCDEGFQLKGSSASYCVLAGMESLWNSSVPVCEQIFCPSPPVIPNG-RHTGKP 2685

Query: 113  IQ---FGSQIKYSCP------KGYRLIGSSSATCII--SGNTVIWDNKTPVC 153
            ++   FG  + Y+C          + LIG S+  C     GN V W +  P C
Sbjct: 2686 LEVFPFGKAVNYTCDPHPDRGTSFDLIGESTIRCTSDPQGNGV-WSSPAPRC 2838


 Score = 37.5 bits (85), Expect = 0.40
 Identities = 33/100 (33%), Positives = 46/100 (46%), Gaps = 17/100 (17%)
 Frame = +1

Query: 54   EFPIGTYLNYECRPGYS-GRPFSII------CLK----NSVWTSAKDKCKRK---SCRNP 99
            + P G  ++Y C      G  F++I      C      N VW+S   +C+     +C +P
Sbjct: 5401 DIPYGKEISYACDTHPDRGMTFNLIGESSIRCTSDPQGNGVWSSPAPRCELSVPAACPHP 5580

Query: 100  PDPVNGM---AHVIKDIQFGSQIKYSCPKGYRLIGSSSATCIISGNTVIWDNKTPVC 153
            P   NG     HV   +  G  I Y+C  GY L+G     C   G   IW      C
Sbjct: 5581 PKIQNGHYIGGHVSLYLP-GMTISYTCDPGYLLVGKGFIFCTDQG---IWSQLDHYC 5739


 Score = 37.5 bits (85), Expect = 0.40
 Identities = 33/117 (28%), Positives = 51/117 (43%), Gaps = 21/117 (17%)
 Frame = +1

Query: 37   VPEWLPFARPTNLTDDF------EFPIGTYLNYECRPGYSGRPF-------SIICLKN-- 81
            +P  LP   PT    DF       F  G+ + Y C PG  GR         SI C  N
Sbjct: 1867 IPCGLP---PTIANGDFISTNRENFHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDD 2037

Query: 82   --SVWTSAKDKCKRKSCRNPPDPVNGMAHVIKD----IQFGSQIKYSCPKGYRLIGSSSA 135
               +W+    +C   +   PP+  NG+  ++ D          +++ C  G+ + G
Sbjct: 2038 QVGIWSGPAPQCIIPNKCTPPNVENGI--LVSDNRSLFSLNEVVEFRCQPGFVMKGPRRV 2211

Query: 136  TCIISGNTVIWDNKTPVC 153
             C        W+ + P C
Sbjct: 2212 KCQALNK---WEPELPSC 2256


 Score = 37.5 bits (85), Expect = 0.40
 Identities = 33/117 (28%), Positives = 51/117 (43%), Gaps = 21/117 (17%)
 Frame = +1

Query: 37  VPEWLPFARPTNLTDDF------EFPIGTYLNYECRPGYSGRPF-------SIICLKN-- 81
           +P  LP   PT    DF       F  G+ + Y C PG  GR         SI C  N
Sbjct: 517 IPCGLP---PTITNGDFISTNRENFHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDD 687

Query: 82  --SVWTSAKDKCKRKSCRNPPDPVNGMAHVIKD----IQFGSQIKYSCPKGYRLIGSSSA 135
              +W+    +C   +   PP+  NG+  ++ D          +++ C  G+ + G
Sbjct: 688 QVGIWSGPAPQCIIPNKCTPPNVENGI--LVSDNRSLFSLNEVVEFRCQPGFVMKGPRRV 861

Query: 136 TCIISGNTVIWDNKTPVC 153
            C        W+ + P C
Sbjct: 862 KCQALNK---WEPELPSC 906


>GSEQ:AAQ11642 Entire human complement type 1 receptor coding
          region.
          Length = 6951
```